ESM-2. Phylogenetic tree generated by Neighbor-Joining analysis based on ITS region sequences describing the relationships of various species and clones of the genus Ceratocystis used in the present study. Bootstrap values (percentages of 1,000 replications) are presented at the node. The outgroup Ophiostoma novo-ulmi sequence was retrieved from the NCBI GenBank under the accession numbers indicated. The scale bar indicates the distance for 10 nucleotides substitutions.